LA-UR-99-6816

USE OF BAYESIAN SOFTWARE TOOLS FOR INTERNAL DOSIMETRY

Chapter 9

Applications of Probability and Statistics in Health Physics
Edited by Thomas B. Borak
Medical Physics Publishing, Madison, Wisconsin, 2000

by

Guthrie Miller
Los Alamos National Laboratory
Los Alamos, NM 87545, U. S. A.

9.1 Introduction

The health physicist concerned with internal dosimetry ultimately desires practical tools to apply to the solution of actual problems encountered on the job. The underlying methodology must be considered valid, but this is not the subject of this chapter. The particular application of Bayesian statistics to internal dosimetry considered here is described in detail in Miller et. al.[1, 2]In this chapter we will use examples of internal dosimetry cases from Los Alamos to demonstrate how Bayesian software tools can be applied to real-life internal dosimetry problems. The Bayesian software package Bayes II for windows systems available from the web site **www.lanl.gov/bayesian** is used. It is assumed that the reader will have downloaded this package and printed the manual describing the UF (Bayesian unfolding) code. In order to reproduce the data plots shown here, the reader needs a copy of the commercial plotting package ORIGIN, although other plotting software could also be used to accomplish the same thing.

Five examples are considered. These examples involve the nuclides Pu-239 and Pu-238. The method applies equally well to any radionuclide, but a library of biokinetic response functions must be available. The Bayes II package includes biokinetic response functions for Pu-239, Pu-238, and Am-241, using ICRP-30 models and ICRP-60 models. We begin by discussing the UF3.1 code.

9.2 THE BAYESIAN UNFOLDING CODE UF3.1

The programs comprising the Bayesian software package (Bayes II) are shown diagrammatically in Fig. 1. The functions of these programs are summarized in Table 1. The files shown in Fig. 1 are

Table 1: Bayesian Internal dosimetry Programs

program	function
UF	Uses bioassay data from the file **urine.in** to calculate possible intakes and doses.
DOSE	Calculates a detailed history of whole body and organ doses using the intake scenario calculated by **UF**.
ORIGIN	A commercially available plotting program used to make a bioassay data versus fit plot from the intake scenario calculated by **UF**.

described in Table 2.

The urine bioassay data and information about incidents is contained in the input data file for the UF code, named URINE.IN. The data files for the five examples considered here are called URINE.111, URINE.222, etc. To calculate for a particular example, copy that urine file into URINE.IN. Another URINE.IN file, called URINE.TST, contains urine bioassay data based on a particular intake scenario (10 nCi intake of class Y 1 mm AMAD Pu-239 by inhalation) on a particular date (2/28/1993) using the ICRP-30 biokinetic model. This simulated data is used as a validation tool since the data corresponds to a known intake. This file is shown in Fig. 2. Using this file as the URINE.IN input file, the terminal output when we run the UF code (by typing "UF" at the command line) is shown in Fig. 3.

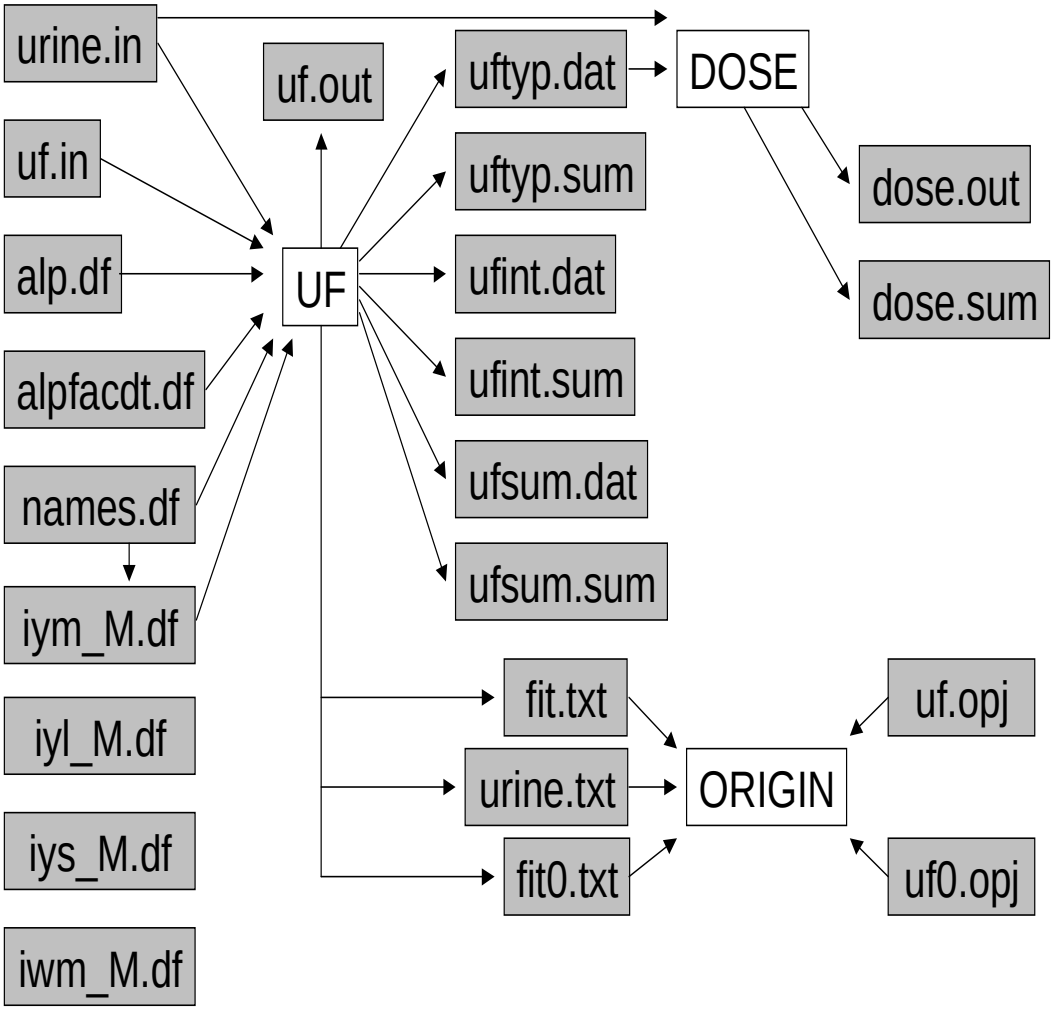

Figure 1: Computer programs to carry out the Bayesian statistical analysis of bioassay data, shown as white boxes, together with input and output files, shown as shaded boxes.

Table 2: Bayesian Internal Dosimetry Program Files

file	description
urine.in	Bioassay data input file.
uf.in	**UF** parameters input file (namelist form).
alp.df, alpfacdt.df	Data files defining intake probability per unit time for non-incident related intakes.
names.df	File defining biokinetic models used.
iym_M.df, iyl_M.df, ...	Biokinetic model data files for all models mentioned in **names.df** for men (**_M**) or women (**_W**).
uf.out	Output file containing everything that appears at the terminal when running **UF**.
uftyp.dat, uftyp.sum	Data files containing intake type information for calculated intakes, records for each intake type for each intake. The **.dat** version contains information for the last time **UF** was run. The **.sum** version appends records. **uftyp.dat** is needed by **DOSE** to calculate detailed dose information.
ufint.dat, ufint.sum	Data files of information about calculated intakes, records for each intake.
ufsum.dat, ufsum.sum	Data files containing summary **UF** output information about all intakes.
uftyp.fld, ufint.fld, ufsum.fld	Single record files containing the field names for the **uftyp**, **ufint**, and **ufsum** data files.
urine.txt, fit.txt, fit0.txt	Files for plotting data. **fit0.txt** contains the fit after the first iteration (normally not used).
uf.opj	**ORIGIN** project file allowing one mouse click plotting of data. Don't delete the dark rectangle in the worksheet, it's important in automatically importing data.
dose.out	File containing terminal output from program **DOSE**.
dose.sum	Append file containing **DOSE** output information.

```
C:\uf31>type urine.in
                                x
    x here to comment-out line->x
                                x
 If intake is incident related, x
 include incident line:         x
                                x
i 02/28/1993 i   1.e1 2.e0 1.00 x Description of incident here
 where                          x
 i requires biokinetic models   x
    that start with i           x
 1.e1 is median of LN prior     x
 2.e0 is sigma of LN prior      x
 1.00 is prior prob that x>0    x
                                x
 To modify the prior prob of an x
 non-incident intake include:   x
                                x
p 03/02/1993 0.                 x
p 07/01/1993 1.                 x
                                x
 Beginning with the first date  x
 intake probability per unit    x
 time is multiplied by 0,       x
 following the second date, 1.  x
                                x
 This is format of urine data:  x
_________ __________ _________ x ----
 date       result   1 SD       x Biological variability
                                x
Test-Urine data 10nCi Inhalationx
 intake of class Y, Medium part x
 size (1 micron AMAD), Pu-239   x
 CEDE is 2.87 rem using ICRP30  x
123456M     IDsex
12/31/1999  ENDCALC
.037        bioassay unit(Bq)
37.         intake unit(Bq)
.01         dose unit(Sv)
i 02/28/1993 iym 1.e1 2.e0 1.00   Inhalation incident
01/01/1993 .0        .0035        0.3
03/01/1993 .1174     .0035        0.3
03/02/1993 .0729     .0035        0.3
03/04/1993 .0325     .0035        0.3
03/08/1993 .0141     .0035        0.3
03/16/1993 .01034    .0035        0.3
04/01/1993 .00854    .0035        0.3
05/01/1993 .00713    .0035        0.3
07/01/1993 .00692    .0035        0.3
11/01/1993 .00746    .0035        0.3
```

Figure 2: Bioassay data input file for code validation case.

```
ZCFAC =   0.100000,
ZMINFAC =   1.000000E-03,
FACNEG =   2.00000,
NI1 =   0,
NDFITPLT =   30,
FACINT =   1.000000E-10,
EPS =   1.000000E-06,
DEFSD =   1.000000E-03,
EXMIN =  -708.000,
EPSL =   5.000000E-02,
EPSU =   5.000000E-02,
ERRTOL =   2.0000000000000000E-003,
$END
 using default prl, prl(1)=pfac, others=1
incidents:
inc date  type a      s       prob description
 2/28/1993 IYM 1.E+01 2.E+00 1.00 Inhalation incident
no intake probability factors
PU-239 half life=   2.411E+04
 number organs or tissues=  5
 most affected body organ=BONE_SURFACE
max fractional difference between ulin and uk(ik(k))=0.0168 for k= 21999
 fit file written:fit0.txt
 fit file written:fit.txt
Data with same date combined
    sample date     result +-  1SD       Bvar Inc? xcrit Prior(x > xcrit)
   1  1/ 1/1993  0.000E+00 +-  3.500E-03 0.30 F 0.00E+00 0.00E+00
   2  3/ 1/1993  1.174E-01 +-  3.500E-03 0.30 T 2.98E-02 9.98E-01
   3  3/ 2/1993  7.290E-02 +-  3.500E-03 0.30 F 5.55E-01 2.37E-05
   4  3/ 4/1993  3.250E-02 +-  3.500E-03 0.30 F 2.49E-01 5.18E-05
   5  3/ 8/1993  1.410E-02 +-  3.500E-03 0.30 F 1.76E-01 1.07E-04
   6  3/16/1993  1.034E-02 +-  3.500E-03 0.30 F 2.73E-01 2.05E-04
   7  4/ 1/1993  8.540E-03 +-  3.500E-03 0.30 F 4.43E-01 3.89E-04
   8  5/ 1/1993  7.130E-03 +-  3.500E-03 0.30 F 4.75E-01 7.24E-04
   9  7/ 1/1993  6.920E-03 +-  3.500E-03 0.30 F 5.34E-01 1.45E-03
  10 11/ 1/1993  7.460E-03 +-  3.500E-03 0.30 F 6.42E-01 2.86E-03
bioassay unit= 3.700E-02 Bq
intake unit= 3.700E+01 Bq
dose unit= 1.000E-02 Sv
        Chisq0/ndat=  168.8690
        Chisq/ndat=    0.0240
int no  1:intake date: 2/28/1993 incident?:I
          data block=   2  10 Chisq/  9=  0.139
          most probable model:IYM Prob model= 1.000
          Prob intake(x > 2.4E-02)= 1.000
          intake amount=9.4E+00 (7.6E+00,9.3E+00,1.1E+01)
          CEDE=2.8E+00          (2.3E+00,2.8E+00,3.4E+00)
          OrganCDE=2.8E+01      (2.3E+01,2.8E+01,3.4E+01)
total CEDE =2.8E+00 +- 3.6E-01
annual dose=7.7E-02 +- 9.8E-03 for year ending 12/31/1999
 ID=123456
program uf, version=3.1 ( 1/24/2000, file size=  349184 bytes)
date of calculation= 1/25/2000
models=ICRP30
elapsed time(min)=      0.03

C:\uf31>
```

Figure 3: Terminal output after running **UF** (also appears in file UF.OUT).

The UF output will now be discussed in some detail. The output begins with a listing of the input parameters. If some parameters have not been specified in the input file UF.IN, this shows the default values used. A description of input parameters is given in Tables 3 and 4.

Table 3: **UF** input parameters

parameter	description
probc	The critical intake probability. The final intake scenario only includes intakes whose posterior probability exceeds **probc**.
bvardef	Default value of biological/sample collection variability used if the data field in the file **urine.in** is zero or blank.
bvfac	A factor applied to all biological/sample collection variabilities, used to investigate the effect of changes of this quantity.
consterr	A logical variable that if true means that the biological variability is incorporated into a constant uncertainty to replace the measurement uncertainty $\sigma = \sqrt{\sigma_m^2 + (B_v y)^2}$, where σ_m is the measurement uncertainty standard deviation, B_v =**bvfac** is the biological variability, and y is the measured value.
pfac	A parameter defining the relative prior probability of the preferred biokinetic model (the first model listed in the file **names.df**).
alpfac	A multiplicative factor applied uniformly to the paramter α in the prior probability of an intake per unit time for non-incident intakes ($\alpha(t)$ is specified by the input files **alp.df** and **alpfacdt.df**).
xmaxni	The maximum value of intake x for non-incident-related intakes in the gamma distribution model (should be larger than the largest conceivable intake).
ani	The parameter a in the gamma distribution $f(x) \propto x^{\alpha \Delta t - 1} \exp\left(-\frac{x}{a}\right)$ used as the prior probability distribution for non-incident-related cases.
xcrit	If **xcrit** is greater than zero it is the parameter $x_{\rm crit}$ defining "positive" as $x > x_{\rm crit}$. If **xcrit** is zero, $x_{\rm crit}$ is **zcfac** times the standard deviation of the likelihood function for zero measured amount.
zminfac	The lower limit of integration over the prior probability distribution for non-incident situations is given by **zminfac** $\times\ x_{\rm crit}$.

Table 4: More **UF** input parameters

parameter	description
facneg	Corrects a problem with data values that are many standard deviations negative. The uncertainty standard deviation of a data point is increased if the result is more than **facneg** standard deviations negative.
ni1	Affects plotting of data only. If a plot is required that has the zero of the time variable at the time of the **ni1**$^{\text{th}}$ incident, set **ni1** equal to the sequence number of the desired incident, otherwise set **ni1** to 0.
ndfitplt	number of days separating calculated expected values of urine excretion in the plot files **fit.txt** and **fit0.txt**. For a short half-life nuclide like tritium, 1 is used. For long half-life nuclides like Pu-239, 30 is sufficient.
facint	The integrations over the prior for an incident are truncated when the log normal drops below **facint** times its maximum value.
eps	A parameter defining the numerical accuracy of integrations.
defsd	The default uncertainty standard deviation of data to be used when this field in the input file **urine.in** is zero or blank.
exmin	The minimum value of the exponent allowed in a double precision number. Used to prevent numerical underflows.
epsl	Usually 0.05, defines the lower credible limit of the Bayesian posterior probability.
epsu	Usually 0.05, defines the upper credible limit of the Bayesian posterior probability.
errtol	The error tolerance in the determination of credible limits of the posterior probability.

Next in the UF output listing is a message stating that the prior probabilities of various intake types (as listed in the NAMES.DF file) are all equal, except that the first is a factor PFAC greater. Following is a list of incidents (potential intake dates). These correspond to lines beginning with "I" in the urine data input file URINE.IN. The incident date is followed by one or more characters that limit the choice of possible biokinetic models. For example an "i" means only inhalations (biokinetic models whose names start with "i"). An "iw" means only class W inhalations (biokinetic models whose names start with "iw"). Other information that appears on the incident line are the log-normal median a = ln(m), the geometric standard deviation $s = \ln(sg)$ [the mean and standard deviation of $\ln(X)$, where X is the input amount], and the prior probability that intake amount is nonzero (not in a delta function at zero). The statement about intake probability factors means that no lines beginning with an "p" were found in the URINE.IN input file that would modify the non-incident probability of an intake as a function of time.

The following lines contain information from the biokinetic model files (those listed in the NAMES.DF file). The isotope name, half life, number of body organs for which doses are calculated, and most affected body organ. The "max fractional difference" gives an indication of interpolation errors in using the biokinetic model data tables. If the tables are smaller, the interpolation errors are larger.

Next are reminders that the fit files FIT0.TXT, after the first iteration and FIT.TXT, after the last iteration, have been written. The "Data with same date combined" statement is a reminder that if two or more bioassay data have the same date, the data are statistically combined. The listed data are the combined resultant data. The (possibly combined) bioassay data are then listed, giving date, measurement result, measurement uncertainty, biological/sample collection variability, "T" or "F", xcrit , and $P[X > X_{crit}]$, where X is the intake amount. The value "T" means an incident occurred in the preceding sampling interval, in which case the potential intake date is the incident date. The value "F" means the potential intake date is the midpoint of the preceding sampling interval. The quantity xcrit defines "positive" [$X > X_{crit}$] after the first iteration. The quantity $P[X > X_{crit}]$ is the prior probability of an intake in the preceding sampling interval using this value of xcrit.

The additional information is mostly self explanatory. The units used for the bioassay measurements, the intake amount, and the dose are given in terms of SI units of Bq and Sv. For the example shown, the units are pCi (0.037 Bq) for bioassay measurement, nCi (37 Bq) for intake amount, and rem (0.01 Sv) for dose. These units are specified in the URINE.IN file.

The different quantities referred to as "Chisq" in the output listing are 1) "Chisq0", the value of c2 assuming no intake, 2) "Chisq", the overall c2?calculated using the Bayesian posterior average intake(s) to calculate the "fit", and 3) the "Chisq" listed with a particular intake, which is the Bayesian posterior expectation value of χ^2/N for the block of data used to determine the intake. Recall that χ^2/N, where N is the number of data points, should be about 1 for a statistically satisfactory fit (asymtotically true for $N \to \infty$, but a useful rough approximation in any case). Smaller than that indicates that the uncertainties used for the bioassay measurements or the biological/sample collection variability are too large, and larger means that the data lies outside the "universe" of possible explanations contained in the family of biokinetic models used, possibly because the data itself are faulty.

The probability of the "most probable" model type referred to in the output listing is the maximum of the Bayesian posterior probability over all the models used to describe this data block. The probability of an intake is the Bayesian posterior probability distribution integrated over all intake amounts larger than xcrit. The expectation value of intake amount is then given followed, in parenthesis, with the lower (EPSL), middle (50%), and upper (EPSU), credible limits of the cumulative Bayesian posterior distribution. The "organ" dose is the committed dose equivalent to the most affected body organ, which is assumed to be the first body organ for which doses are given in the biokinetic model data files.

The biokinetic models used are specified by the file NAMES.DF shown in Fig. 4. The biokinetic model names are defined in this file and associated with biokinetic model data files. The number of times in the interpolation tables NTIMES is arbitrary, although too small a number leads to large interpolation errors. In order to calculate committed doses, the last time value should be at least 18263 days (50 years). It may need to be longer to accommodate very long employment histories over 50 years in length.

```
C:\uf31>type names.df
       This file contains the prefixes of the names of the
       ICRP-30 biokinetic response files *.df (df for Data File),
       containing bioassay projection and dose as a function
       of time following an intake of unit amount of contaminant.
       For example, for Pu, the file IYM.DF contains the urine
       excretion and dose following an acute inhalation of class
       Y, medium particle size (1 micron AMAD) Pu.

       The biokinetic response files contain NTIMES times
       spanning 1 through MAXDAYS days. The response at arbitrary times
       is interpolated. For each time the following data is given:
       time(d), urine(Bq/d), ed(Sv), tissue de(Sv) for NTISSUE tissues
       assuming a 1 Bq intake, where time is the time after the intake.

       The first response file is the default
ntimes_=300
maxdays=21999
ntissue=5
models_=ICRP30
iym
iyl
iys
iwm
iwl
iws
wnd
win
wdt
wta
```

Figure 4: File specifying the biokinetic models used.

A portion of the data file for a particular biokinetic model ("iym_M") is as shown in Fig. 5. There are 300 lines of data, giving urine excretion and dose for various times. Only the last few lines are shown. The lines including and after the "format for above:" line are for documentation only. The quantity NTISSUE gives the number of tissues for which doses are calculated. The program UF uses only the first organ dose. The program DOSE uses all NTISSUE organ doses to calculate detailed dose information.

Two other data files define the prior probability of an intake for non-incident cases. These are shown in Fig. 6.

The ORIGIN plot for this example is shown in Fig. 7. Fig. 8 shows the same data on a log-log scale, where the time variable is now days after intake (incident date) obtained by setting NI1 equal to 1 (the first incident is used to define time zero) in the input parameter file UF.IN.

For this validation case we see that the Bayesian expectation fits the urine data very well, and the calculated dose (CEDE=0.028 Sv) is quite close to the actual value (CEDE=0.0287 Sv).

We now proceed to discussing application of the UF code to real plutonium internal dosimetry problems from Los Alamos.

```
 1.726E+04 4.560E-07 7.846E-05 7.676E-04 3.031E-04 1.465E-04 6.214E-05 1.125E-05
 1.773E+04 4.499E-07 7.962E-05 7.845E-04 3.056E-04 1.484E-04 6.351E-05 1.158E-05
 1.822E+04 4.438E-07 8.080E-05 8.015E-04 3.081E-04 1.502E-04 6.489E-05 1.193E-05
 1.871E+04 4.375E-07 8.199E-05 8.187E-04 3.107E-04 1.521E-04 6.628E-05 1.228E-05
 1.922E+04 4.312E-07 8.319E-05 8.360E-04 3.133E-04 1.539E-04 6.768E-05 1.265E-05
 1.975E+04 4.248E-07 8.441E-05 8.534E-04 3.160E-04 1.556E-04 6.909E-05 1.302E-05
 2.029E+04 4.183E-07 8.564E-05 8.710E-04 3.188E-04 1.574E-04 7.051E-05 1.341E-05
 2.084E+04 4.117E-07 8.689E-05 8.886E-04 3.217E-04 1.590E-04 7.194E-05 1.380E-05
 2.141E+04 4.051E-07 8.815E-05 9.064E-04 3.246E-04 1.607E-04 7.337E-05 1.420E-05
 2.200E+04 3.984E-07 8.942E-05 9.242E-04 3.277E-04 1.623E-04 7.482E-05 1.462E-05
PU-239   2.411E+04 = nuclide half life(years)
ntissue=    5 tissue names and weighting factors:
Bone_Surface           0.030
Lung                   0.120
Liver                  0.060
Red_Marrow             0.120
Gonads                 0.250
 format for above:
 time(d), urine(Bq/d), ede(Sv), tissue de(Sv)
 for 1 Bq intake

 $L
 NUCLIDE = 'PU-239',
 COMMENTS = 'class Y, 1 micron              ',
 MODEL = 'Jones                           ',
 THALF =   24113.0000000000,
 DNP =   0.300000000000000,
 DTB =   8.00000000000000E-002,
 DP =   0.250000000000000,
 TA =   1.00000000000000E-002,
 TB =   0.400000000000000,
 TC =   1.00000000000000E-002,
 TD =   0.200000000000000,
 TE =   500.000000000000,
 TF =   1.00000000000000,
 TG =   500.000000000000,
 TH =   500.000000000000,
 TI =   1000.00000000000,
 TS =   1.00000000000000,
 TSI =   4.00000000000000,
 TULI =   13.0000000000000,
```

Figure 5: Portion of biokinetic model data file.

```
C:\uf31>type alp.df
c data that defines prior prob of
c intake (per yr) as linear function in time
c taking values given for given times
c (c in column 1 means line is ignored)
c
c time       value
cmm/dd/yyyy ----------
c
 01/01/1901 .1
 01/01/1946 .1
 01/01/1947 .01
 01/01/1970 .001

C:\uf31>type alpfacdt.df
c data that defines correction factor
c to prior prob of
c intake (per yr) as function of
c sampling time interval.
c Data defines linear function in time
c taking values given for given times
c (c in column 1 means line is ignored)
c
c t(d) value
c-----________
c
 0   1.
 365  1.
 730  0.
c
c workers not sampled for 2 yrs have
c been working at other jobs without
c prob of intake
c (730d = 2 yr)
```

Figure 6: Data files that define the prior probability of an intake for non-incident cases.

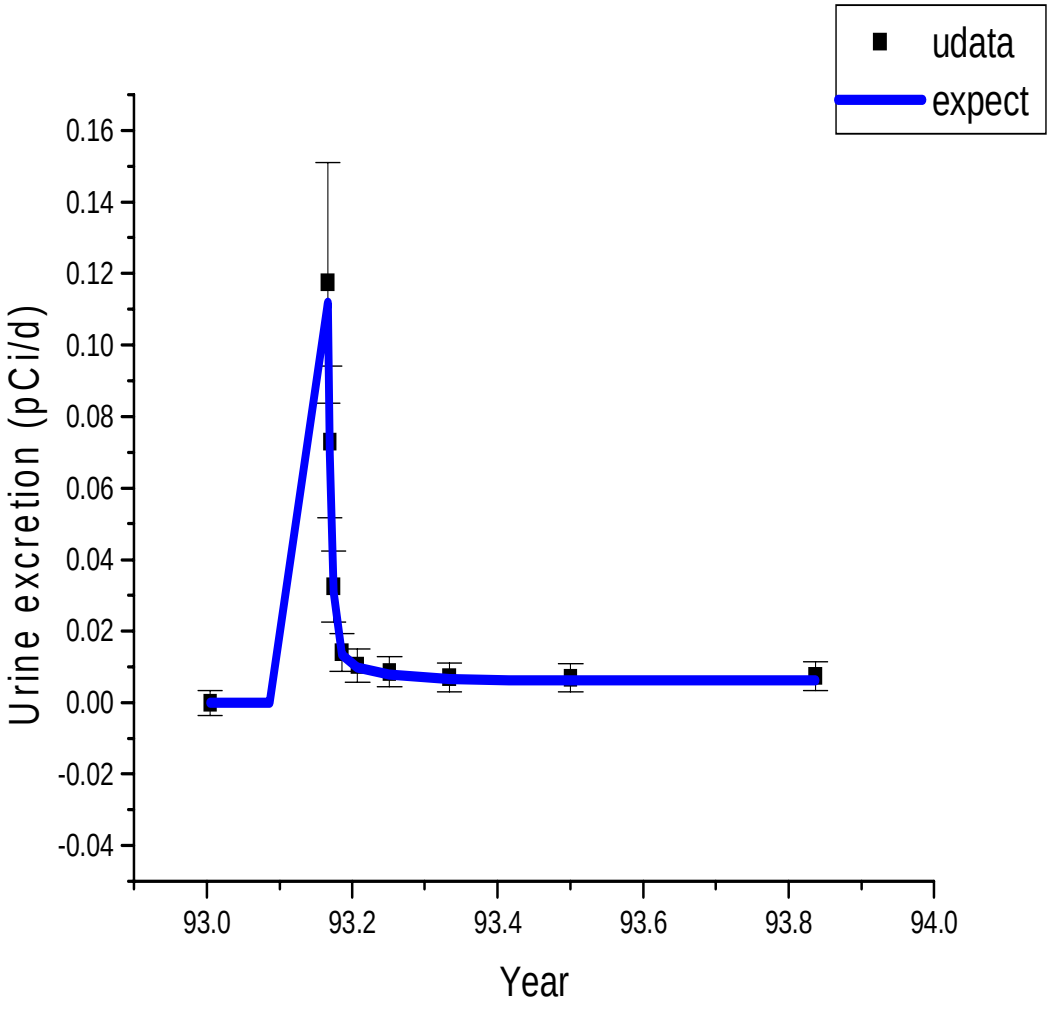

Figure 7: Normal **ORIGIN** plot of bioassay data and "fit".

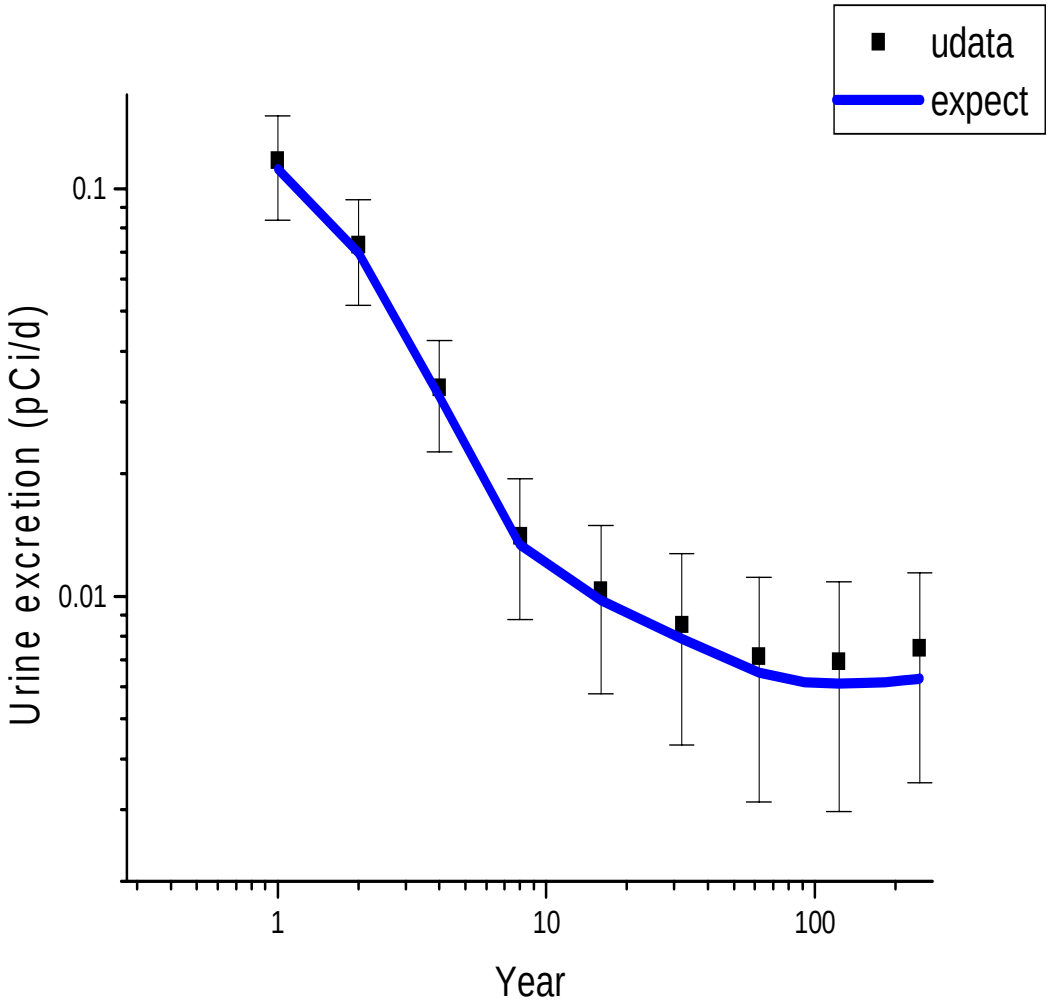

Figure 8: Log-log **ORIGIN** plot of bioassay data and "fit" when **ni1** is nonzero.

9.3 EXAMPLE 1-NON-INCIDENT-RELATED PU-239 INTAKE DETECTED FROM ROUTINE MONITORING

"Incidents" are defined by work-place indicators, for example air monitor alarms, elevated nose swipe results or high external contamination levels. For plutonium, non-incident related intakes are extremely rare (about 1 in 1000 bioassay samples, see Miller et. al.[2], but they do occur. An example is shown in Fig. 9, which shows the PU-239 bioassay history from a Los Alamos worker from 1984 to 1998. The curve "expect" is the expectation value of the urine excretion calculated from the Bayesian posterior probability distribution. The Committed Effective Dose Equivalent (CEDE) for the intake shown in Fig. 9 is 0.11 0.022 Sv (expected value 1SD) . The 5%, 50%, and 95% limits of the posterior distribution are 0.069, 0.11, and 0.14 Sv.

The biokinetic models are drawn from the ICRP-30 set of models as called out in the NAMES.DF file, as has been discussed. There is the option to use ICRP-60 models as well. To set up biokinetic model files for a particular nuclide, for example Pu-239, using ICRP60 models type at the command line

getdfs icrp60 pu239.

The choices are ICRP30, ICRP60 and Pu239, Pu238, and Am241.

Using ICRP-60 rather than ICRP-30, the results are considerably different. The comparison of urine data and expectation value is shown in Fig. 10 using ICRP-60 biokinetic models. The Committed Effective Dose is 0.021 ± 0.006 Sv, with 5%, 50%, and 95% credible limits of 0.017, 0.020, and 0.024 Sv.

The expected value is an average over different types of biokinetic response. For ICRP-30, the most likely response type is class Y, large particle size (5 mm AMAD). For ICRP-60, the most probable response function turns out to be type M, large particle size (10 mm AMAD). This accounts for the factor of 5 discrepancy in the dose. For given urine results, ICRP-60 doses for type S are about a factor of 2 less than those from ICRP-30 class Y, while type M (class W) doses are less than those from type S (class Y).

Note that the lower credible limit of the ICRP-30 dose, 0.069 Sv is quite a bit larger than the upper credible limit of the ICRP-60 dose, 0.024 Sv. This is because the calculated uncertainties do

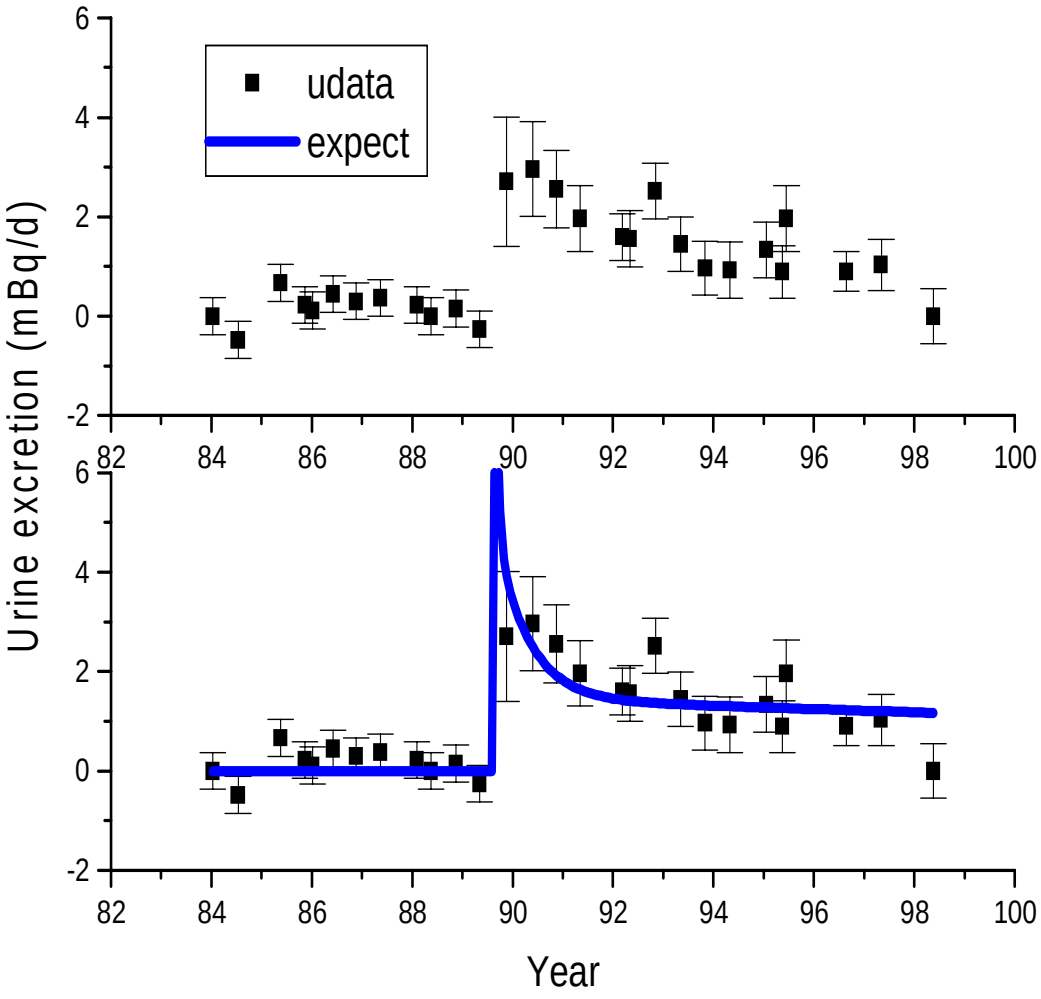

Figure 9: Intake detected using routine monitoring, ICRP-30 biokinetic models.

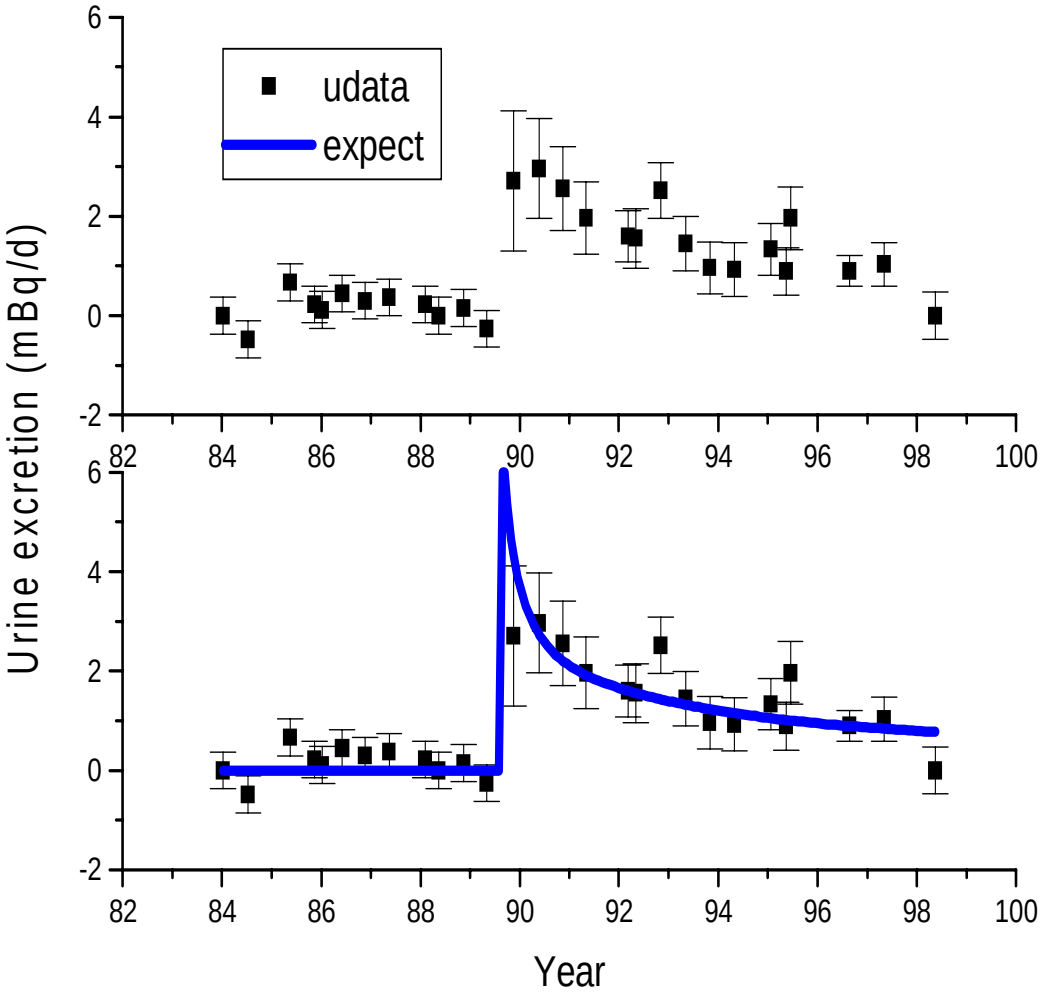

Figure 10: Intake detected using routine monitoring, ICRP-60 biokinetic models.

not include an uncertainty associated with the family of biokinetic models. This source of uncertainty could be taken into account using the Bayesian method, and it would be reasonable to calculate a posterior probability of ICRP-30 relative to ICRP-60 based on the goodness of fit of models within each family to the urine excretion data. A prior probability could be used to relatively weight ICRP-30 compared to ICRP-60. The calculated uncertainty would then involve an average over different families of models and would be significantly larger.

9.4 EXAMPLE 2-INCIDENT-RELATED PU-239 INTAKE

In this 1993 case there were high-level work place indicators that an intake had occurred, a CAM alarm and nose swipe results of 366 dpm / 814 dpm. The individual had been involved in two previous incidents, but whether or not these incidents had resulted in intakes was not completely clear, although the individual was clearly excreting plutonium from a previous intake or intakes, whether or not these were incident related. The data and ICRP-30 UF interpretation are shown in Fig. 11. There are two incident-related intakes in this interpretation of the data. The 1993 intake resulted in a CEDE of 0.14 Sv. If we switch to ICRP-60 biokinetic models, the earlier intakes are not incident related as shown in Fig. 12. The expected value curve now has an increased width reflecting the uncertainty of the background caused by the earlier intakes. The 1993 CED becomes 0.051 Sv, still an overexposure.

For the ICRP-60 interpretation, the probabilities of the three intakes are 0.85, 0.596, and 1.00. Normally we would like the intake probabilities to all be nearly 1, and the 0.596 probability is low. The odds that an intake actually occurred are only 0.596/(1.-0.596) = 1.47 to 1. The UF code parameter PROBC (specified in the UF.IN file) defines the lowest probability allowed for an intake. If we change the value of this parameter from 0.5, as it was for Fig. 12, to 0.6, the result shown in Fig. 13 is obtained. There are now two intakes, both with probability of intake 1.00. The 1993 CED is now 0.062 Sv.

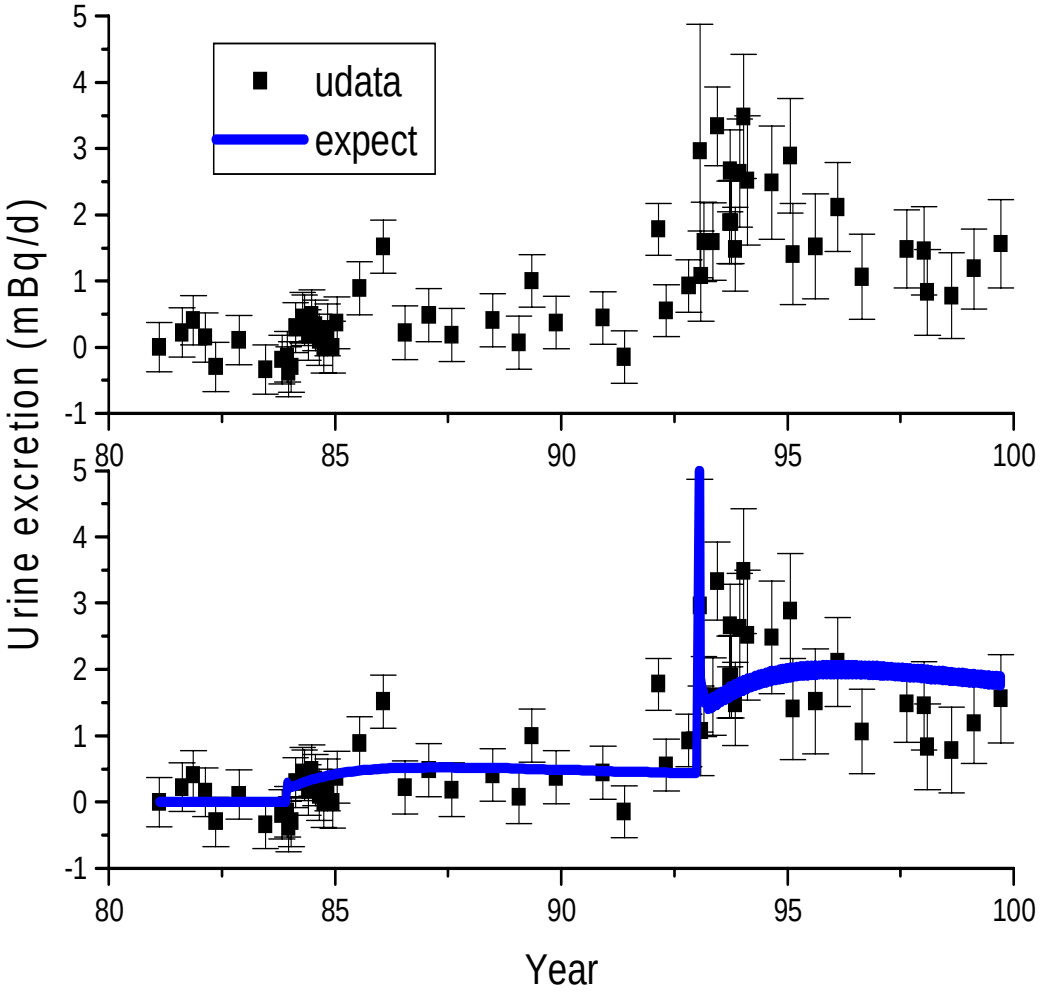

Figure 11: Intake resulting from 1993 incident, ICRP-30 biokinetic models.

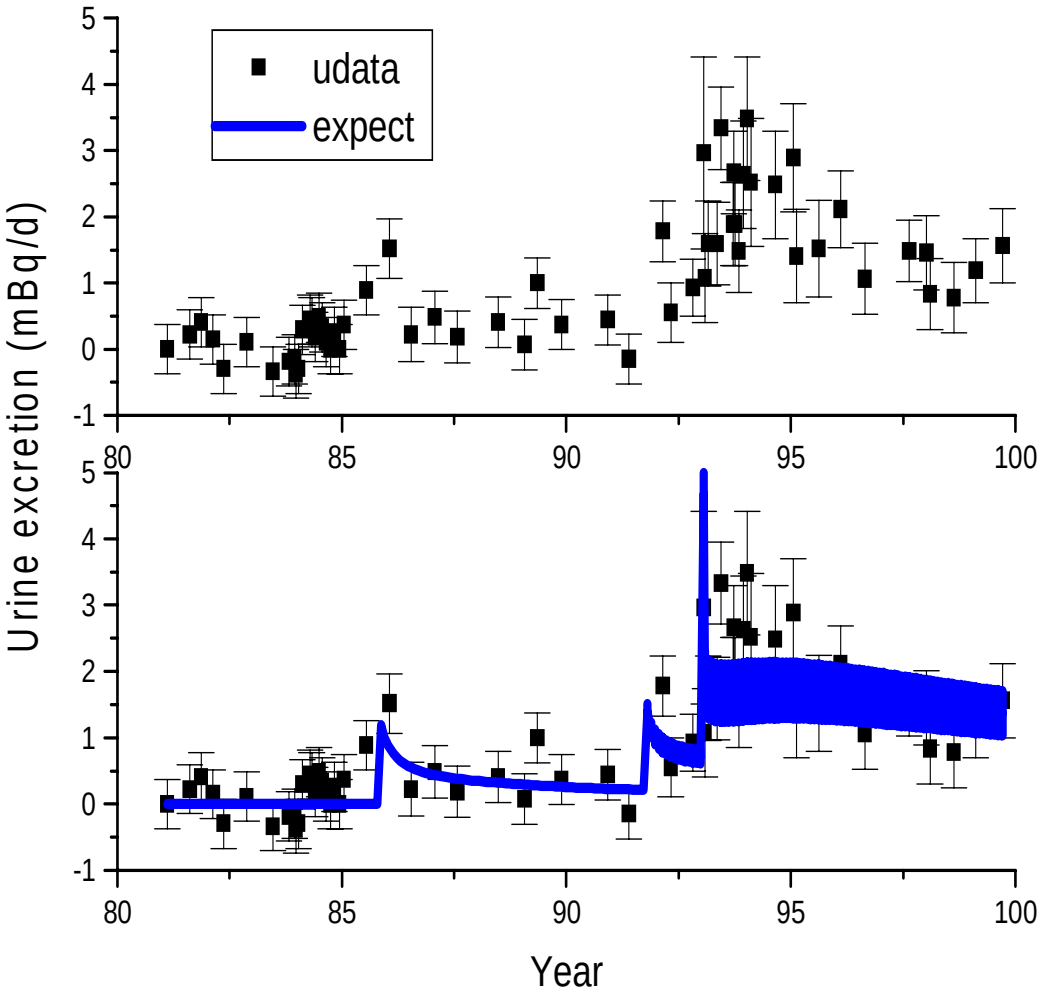

Figure 12: Intake resulting from 1993 incident, ICRP-60 biokinetic models.

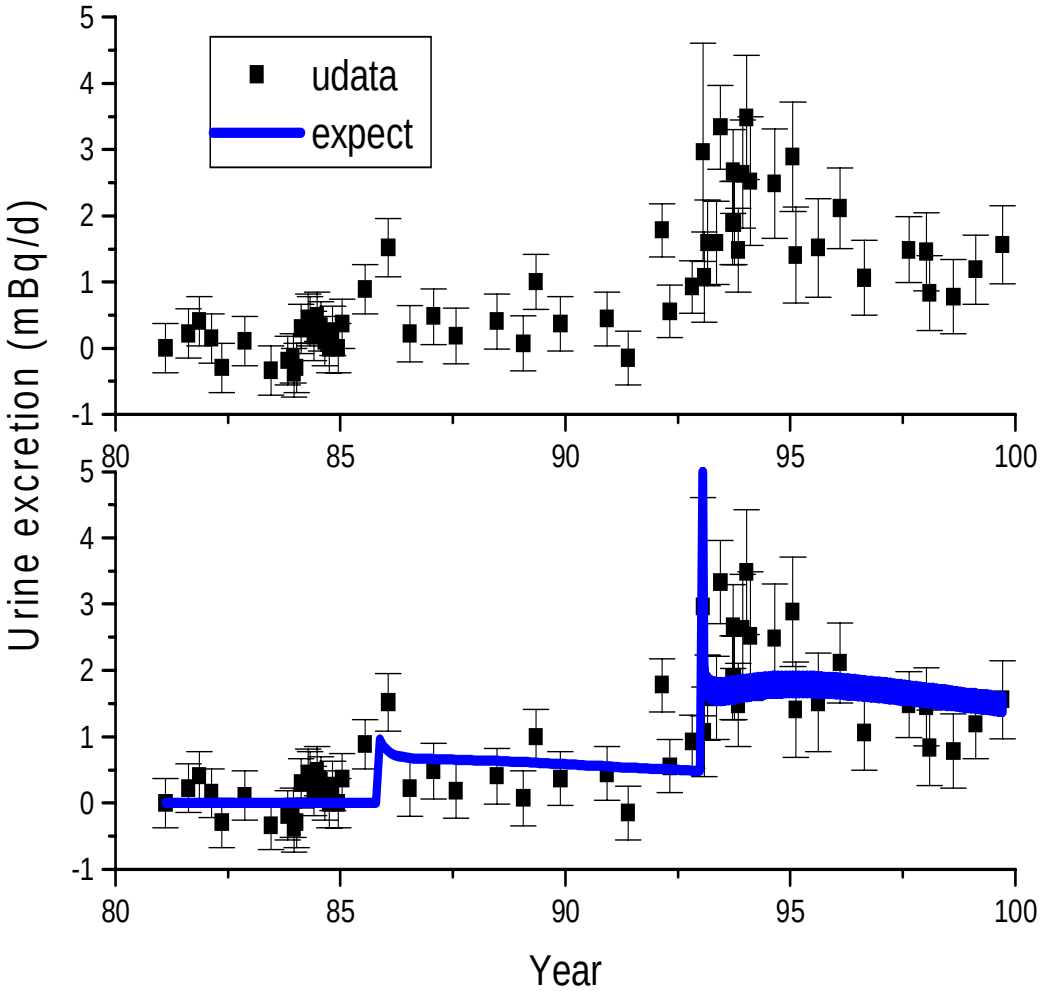

Figure 13: Intake resulting from 1993 incident, ICRP-60 biokinetic models, limiting intake probability increased to 0.6.

9.5 EXAMPLE 3-MULTIPLE PU-238 INTAKES

In this example there are three intakes, none of them incident related. The urine excretion data and ICRP-30 interpretation are shown in Fig. 14. The ICRP-60 interpretation is shown in Fig. 15. Remember to type

getdfs icrp30 pu238

to set up the biokinetic model files for Pu-238.The CEDE's and most probable biokinetic responses are shown in Table 5. Note that

Table 5: Multiple intakes interpreted using ICRP-30 and ICRP-60

ICRP-30			
intake year	CEDE(Sv)	class	AMAD(μm)
1980	0.12	Y	1
1981	0.15	Y	5
1987	0.12	Y	5
ICRP-60			
intake year	CED(Sv)	type	AMAD(μm)
1980	0.052	S	5
1981	0.16	S	10
1987	0.024	M	1

both ICRP-30 and ICRP-60 models identify the same intake times-a good indication! Although the calculated uncertainties include many components, missing is the uncertainty associated with the nonlinear UF code deciding to interpret data with a different intake scenario, in effect saying "no the intake doesn't occur there, it occurs here". An example of this has been already seen in example 2. A full straight forward Bayesian treatment of the internal dosimetry problem rather than an unfolding technique would remedy this situation, as discussed in Miller et. al.[1], although it seems presently to be not feasible because of the high dimensional integrations involved.

9.6 EXAMPLE 4-PU-239 OVEREXPOSURE DETECTED FROM ROUTINE MONITORING

This case attracted attention recently. The data and ICRP-30 interpretation are shown in Fig. 16. The first elevated urine result from

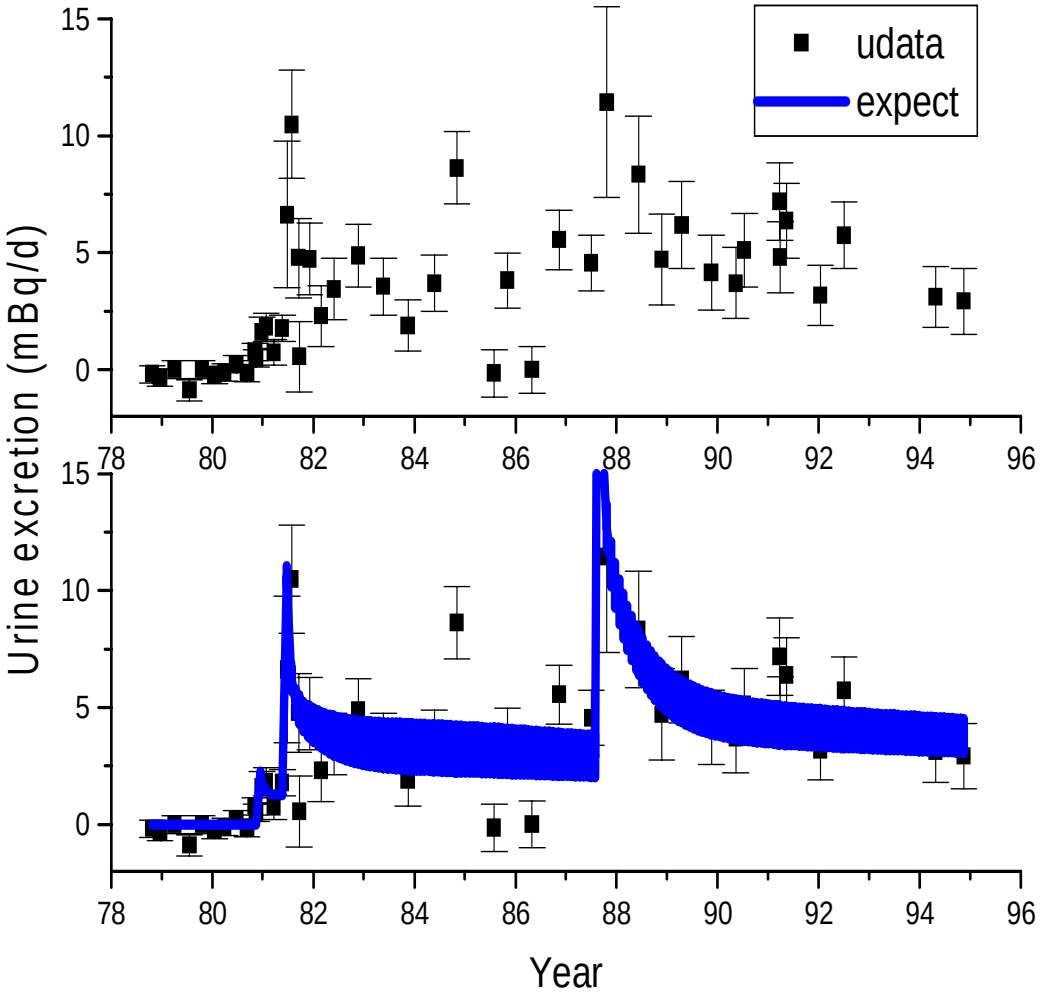

Figure 14: Multiple PU-238 intakes, ICRP-30 biokinetic models.

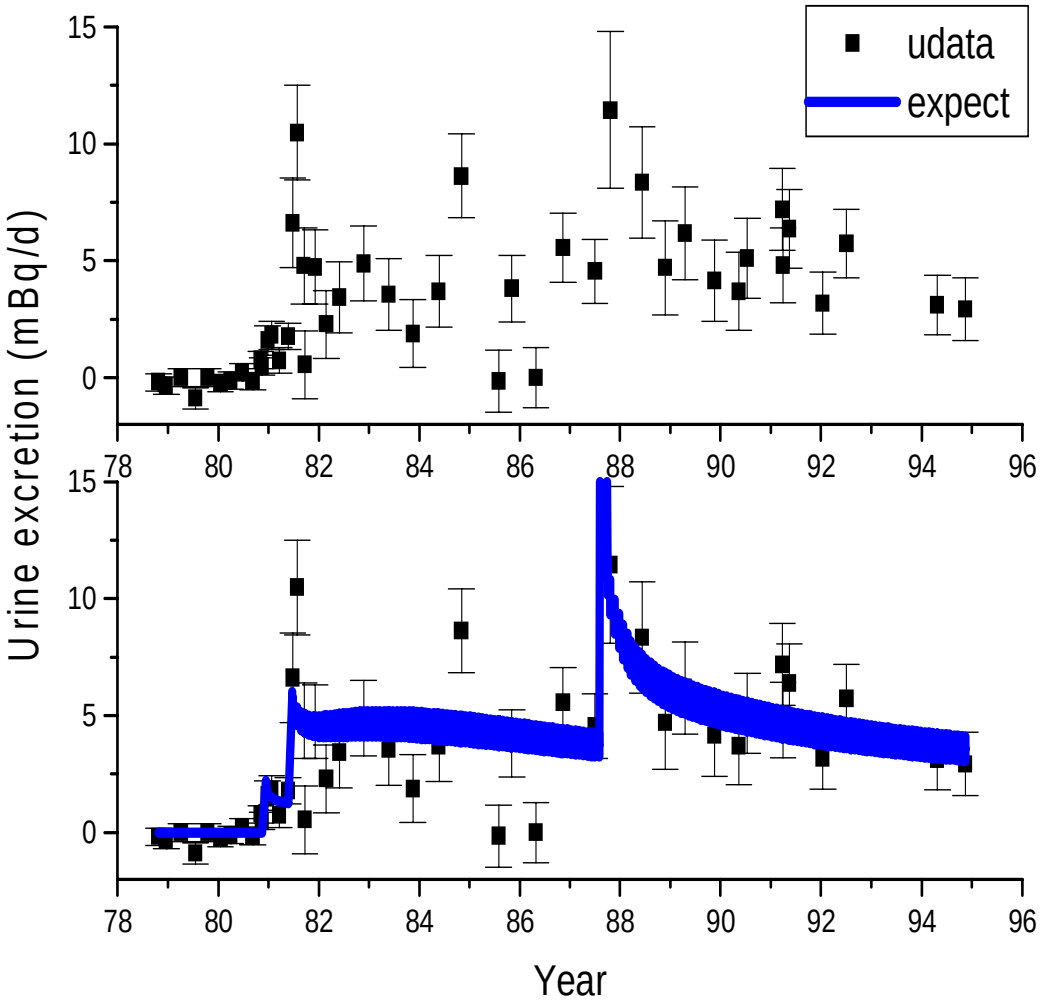

Figure 15: Multiple PU-238 intakes, ICRP-60 biokinetic models.

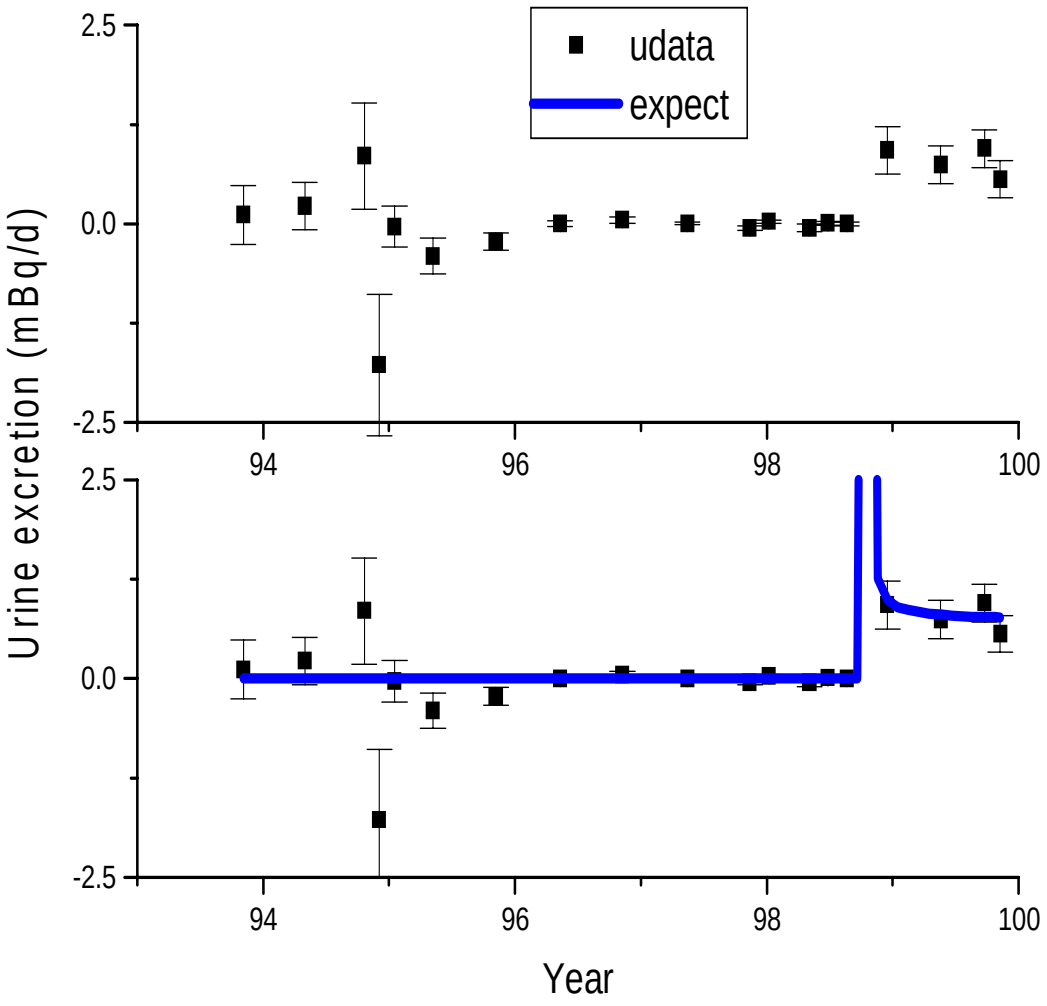

Figure 16: PU-239 overexposure detected from routine urine monitoring.

December 1998 did not trigger a resample, since the intake probability was only 21%, below the 50% cutoff. Normally high results are followed up by resampling when the intake probability exceeds 50%, and dose results are reported when enough data has been accumulated to have the intake probability be nearly 1. Table 6 shows

Table 6: PU-239 overexposure detected from routine urine monitoring– evolution of statistical bounds on dose as more data is accumulated.

Collected date	analysis type	Prob of intake	CEDE(Sv) expected	5%	50%	95 %
12/15/1998	RAS	21 %	0.02	0	0	0.16
5/19/1999	RAS	86 %	0.032	0	0.011	0.12
9/22/1999	RAS	99.8%	0.065	0.008	0.055	0.16
9/22/1999	TIMS	100 %	0.073	0.014	0.077	0.14
11/7/1999	RAS	100 %	0.065	0.014	0.067	0.12

the time progression of our knowledge of this intake after each data point. The expected dose and 5%, 50%, and 95% credible limits are shown. The elevated urine result was obtained by Radiochemical Alpha Spectrometry (RAS), but it was preceded by a higher sensitivity result obtained by Thermal Ionization Mass Spectrometry (TIMS) so the time of intake is bracketed between 19-August-1998 and 15-December-1998. Using ICRP-60, the CED is 0.029 Sv.

We note that up until now the calculated TIMS measurement uncertainties have been somewhat arbitrarily increased over their nominal values using the calculation $\sigma \rightarrow \sqrt{\sigma^2 + \sigma_0^2}$, where $\sigma_0 = 15$ μBq, pending studies of the distribution of data for urine blanks. We have now implemented a system of continuously tracking the distribution of urine blanks as a quality assurance measure, and such a correction would have σ_0 in the range of 2-4 μBq.

9.7 EXAMPLE 5-PU-238 1999 INTAKE RULED OUT BY PRIOR

In this case an individual who had had a previous intake had two elevated urine results in 1999, seeming to imply another intake in 1999. However the individual had transferred to another job outside the plant in 1994 and as a result of this transfer had a greatly reduced prior probability of intake. The ICRP-30 interpretation shown in Fig. 17 has a prior probability factor of 1/10 applied beginning 1-

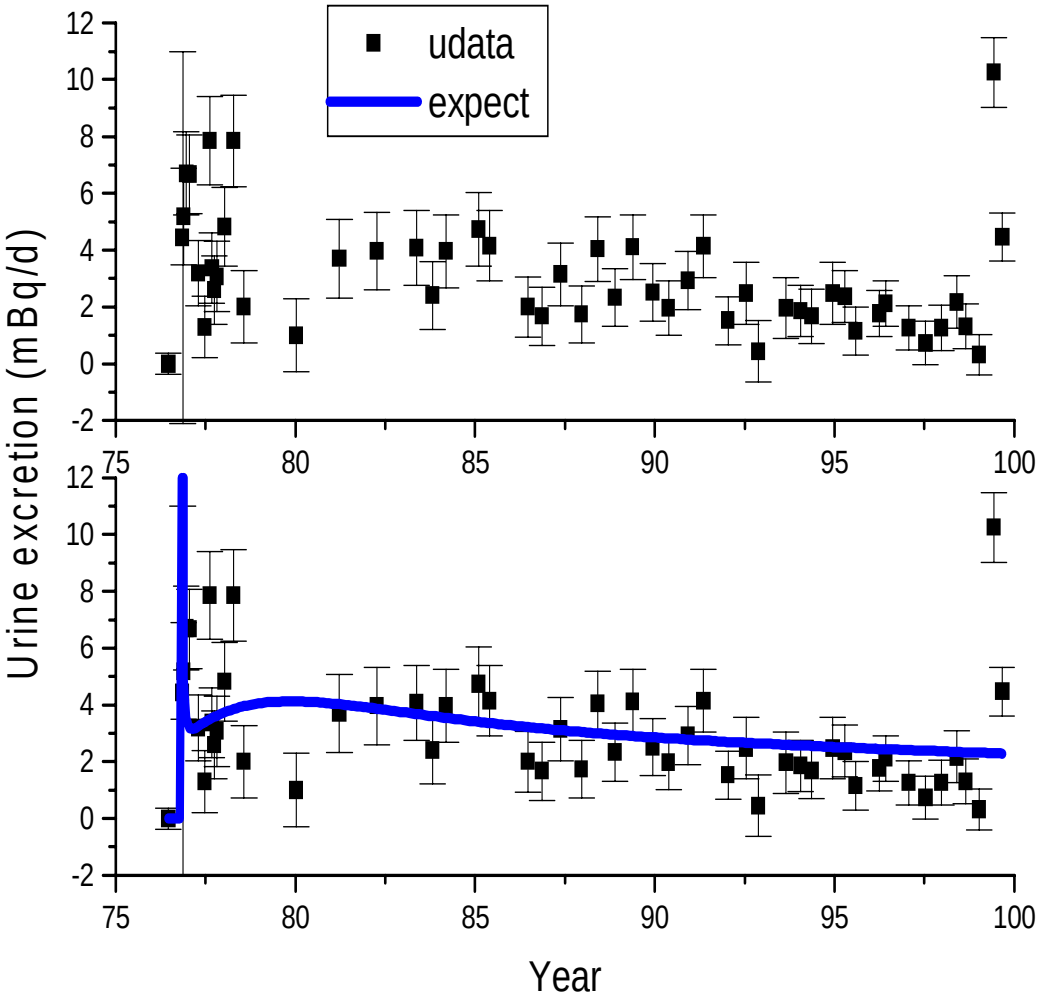

Figure 17: PU-238 intake in 1999 ruled out by prior.

January-1994. Such a modification of the prior probability of an non-incident-related intake is specified in the UF code by lines in the URINE.IN file beginning with a "p" (as in the URINE.555 file). With this factor, there is no 1999 intake. Without it (or with the input line commented out), there is a 1999 intake of 0.24 Sv. The higher than normal excretion of plutonium may have been caused by medications the individual was taking, but we have no clear understanding of its cause.

References

[1] G. Miller, W. C. Inkret, and H. F. Martz. Internal Dosimetry Intake Estimation Using Bayesian Methods. *Radiation Protection Dosimetry*, 82:5–17, 1999.

[2] G. Miller, W. C. Inkret, T. T. Little, H. F. Martz, and M. E. Schillaci. Bayesian Prior Probability Distributions for Internal Dosimetry. *Radiation Protection Dosimetry* (to appear). LA-UR-99-5279.